

FIGURE 1
Map of a First IL-17 Receptor Like cDNA (SEQ ID No: 1)
and Amino Acid (SEQ ID NO: 2)

1 ATAAAAGCGCAGCGTGC GGGTGGCCTGGATCCCCGCGCAGTGGCCCCGGCGATGTCGCTCGT 60
M S L V -

61 GCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCCGAGAGCCGACCGTTCAATG 120
L L S L A A L C R S A V P R E P T V Q C -

121 TGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCCGGAGA 180
G S E T G P S P E W M L Q H D L I P G D -

181 CTTGAGGGACCTCCGAGTAGAACCTGTTACAAC TAGTGTGCAACAGGGGACTATTCAAT 240
L R D L R V E P V T T S V A T G D Y S I -

241 TTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTGTAAGGCCAC 300
L M N V S W V L R A D A S I R L L K A T -

301 CAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCTGTGTGAGGTGCAATTA 360
K I C V T G K S N F Q S Y S C V R C N Y -

361 CACAGAGGCCCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCCTACAT 420
T E A F Q T Q T R P S G G K W T F S Y I -

421 CGGCTTCCCTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCCATAATATTCCTAATGC 480
G F P V E L N T V Y F I G A H N I P N A -

481 AAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGA 540
N M N E D G P S M S V N F T S P G C L D -

541 CCACATAATGAAATATAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACAT 600
H I M K Y K K K C V K A G S L W D P N I -

601 CACTGCTTGTAAGAAGAATGAGGAGACAGTAGAAGTGAAC TTCACAACCACTCCCCTGGG 660
T A C K K N E E T V E V N F T T T P L G -

661 AAACAGATACATGGCTCTTATCCAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGA 720
N R Y M A L I Q H S T I I G F S Q V F E -

721 GCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGA 780
P H Q K K Q T R A S V V I P V T G D S E -

781 AGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGCAGCGACTGCATCCGACA 840
G A T V Q L T P Y F P T C G S D C I R H -

841 TAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAA 900
K G T V V L C P Q T G V P F P L D N N K -

901 AAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGT 960
S K P G G W L P L L L L S L L V A T W V -

961 GCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTTTC 1020
L V A G I Y L M W R H E R I K K T S F S -

1021 TACCACCACACTACTGCCCCCATTAAAGTTCTTGTGGTTTACCCATCTGAAATATGTTT 1080
T T T L L P P I K V L V V Y P S E I C F -

1081 CCATCACACAATTTGTTACTTCACTGAATTTCTTCAAACCAATTGCAGAAGTGAGGTCAT 1140
H H T I C Y F T E F L Q N H C R S E V I -

1141 CCTCGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCAC 1200
L E K W Q K K K I A E M G P V Q W L A T -

09340927 034604
T09T20 2250T2860

Figure 1 (continued)

1201 TCAAAAGAAGGCAGCAGACAAAGTCGTCTTCCTTCTTTCCAATGACGTCAACAGTGTGTG 1260
Q K K A A D K V V F L L S N D V N S V C -

1261 CGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCC 1320
D G T C G K S E G S P S E N S Q D L F P -

1321 CCTTGCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTTCATCTGCACAAATACGT 1440
L A F N L F C S D L R S Q I H L H K Y V -

1441 GGTGGTCTACTTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCC 1500
V V Y F R E I D T K D D Y N A L S V C P -

1501 CAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCA 1560
K Y H L M K D A T A F C A E L L H V K Q -

1561 GCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTGTAGCC 1620
Q V S A G K R S Q A C H D G C C S L *

1621 CACCCATGAGAAGCAAGAGACCTTAAAGGCTTCCTATCCCACCAATTACAGGGAAAAAAC 1680

1681 GTGTGATGATCCTGAAGCTTACTATGCAGCCTACAAACAGCCTTAGTAATTAAAAACATTT 1740

1741 TATACCAATAAAATTTTCAAATATTGCTAACTAATGTAGCATTAACTAACGATTGGAAAC 1800

1801 TACATTTACAACCTTCAAAGCTGTTTTATACATAGAAATCAATTACAGCTTTAATTGAAAA 1860

1861 CTGTAACCATTTTGATAATGCAACAATAAAGCATCTTCAGC 1901

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1 .....MSLVLLSLAALCRSAVPREP 20
1 MGAARSPPSAVPGPILLGLLLLLLGV LAPGGASLRLLDHRALVCSQPGLNC 50
21 TVQCGSETGPSPEWMLQHDLIPGDLRLDRVEPVTTTSVATGDYSILMNVSW 70
|| . . | . | . | : || : : || . . : |
51 TVK..NSTCLDDSWIHPRNLTPSSPKDLQIQLFHAHTQQGDLFPVAHIEW 98
71 VLRADASI RLLKATKICVTGKS NFQS YSCVR CNYTEAFQTQTRPSGGKW T 120
| . ||| | . : | . | ||| | . | : |
99 TLQTDASILYLEGAELSVLQLNTNERLCVRFE...FLSKLRHHHRRWR 143
121 FSYIGFPELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYK 170
|. : | |: | : |: | : | | | | | |
144 FTFSHFVVDPDQEYEVT VHHL PKPI PDGDP NHQSKNFLVPDCEHARMKV T 193
171 KKC VKAGSL WDPNITACKKNEETVEVNFTTTPLGNRYMALI.....QH 213
| . . ||| | | | | | . | . || | | : |
194 TPC MSSGS LWDPNITVETLEAHQLRVSFTLWNESTHYQILLT SFPHMEN H 243
214 STIIGFSQVFEPHQKKQTRASVVIPVTGDSEGA...TVQLTPYFPTCGSD 260
| : | : | . . | | | . | | : : | : | . | . |
244 SCFEHMHHIPAPRP EEFHQRS NVTLTLRN LKGCCR HQVQIQPF FSSCLND 293
261 CIR HKGT VVLCPQ.TGV PFFLDNNK SKPGGWLP LLLL SLLVATWVLVAG I 309
| : | | | | : | | : . | : : : | : : :
294 CLRHSAT.VSCP EMPDTPEPIP DYMP LWVYW F.ITGIS ILLVG SVILLIV 341
310 YLMWRHERIKKTSFSTTT.....LLP....PIKVLVVYPSE.ICF 344
: || : | | : | | | : | : : :
342 CMTWRLAGPGSEKYSDDTKYTDGLPAADLI PP LKPRK VWIIYSADHP LY 391
345 HHTICYFTEFLQNHC RSEVILE KWQKKKIAEMGPVQWLATQK...KAAD 390
: | : | | | . || : : . . | . | . | | ..
392 VD VVLKFA QFLLTACGTEVALDLL EEQAISEAGVM TWVGRQKQ EMVESNS 441
391 KV VFLLSNDV NSVC DGT CGKSEG SP.....SENSQDLF PLAFNLFC SD 433
| : : | | : | : | . | | | | | : |
442 KI IV LCSRG TRAKWQALLGR..GAPV RLRC DHGK PVGD LF TAAMNM ILPD 489
434 LRSQIHLHKYVVVYFREIDTKDDY.NALSVC PKYHLMK..DATAFCAELL 480
: | | | | | : | . | : | | : | : |
490 FK RPACFGTYVVCYF SEVSCDG DV PDLFGAA PRYPLMDRFEEVYFR IQDL 539
481 HVKQQVSAGKRSQACHDGCSSL*..... 503
540 EMFO PG RMHRV GELSGDN YLRSPG GRQLRAAL DRFRDWQVR CPDWFECEN 589

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Figure 3 (continued)

1021 AACAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAAAAGCAA 1080
T V V L C P Q T G V P F P L D N N K S K -

1081 GCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGT 1140
P G G W L P L L L L S L L V A T W V L V -

1141 GGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCAC 1200
A G I Y L M W R H E R I K K T S F S T T -

1201 CACACTACTGCCCCCATTAAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCATCA 1260
T L L P P I K V L V V Y P S E I C F H H -

1261 CACAATTTGTTACTTCACTGAATTTCTTCAAACCATTGCAGAAGTGAGGTCATCCTCGA 1320
T I C Y F T E F L Q N H C R S E V I L E -

1321 AAAGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAA 1380
K W Q K K K I A E M G P V Q W L A T Q K -

1381 GAAGGCAGCAGACAAAGTCGTCTTCCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGG 1440
K A A D K V V F L L S N D V N S V C D G -

1441 TACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGC 1500
T C G K S E G S P S E N S Q D L F P L A -

1501 CTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTTCATCTGCACAAATACGTGGTGGT 1560
F N L F C S D L R S Q I H L H K Y V V V -

1561 CTACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTA 1620
Y F R E I D T K D D Y N A L S V C P K Y -

1621 CCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGT 1680
H L M K D A T A F C A E L L H V K Q Q V -

1681 GTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTGTAGCCCACCCA 1740
S A G K R S Q A C H D G C C S L *

1741 TGAGAAGCAAGAGACCTTAAAGGCTTCCTATCCCACCAATTACAGGGAAAAAACGTGTGA 1800

1801 TGATCCTGAAGCTTACTATGCAGCCTACAAACAGCCTTAGTAATTAACATTTTATACC 1860

1861 AATAAAATTTTCAAATATTGCTAACTAATGTAGCATTAACTAACGATTGGAACTACATT 1920

1921 TACAACTTCAAAGCTGTTTTATACATAGAAATCAATTACAGCTTTAATTGAAAAGTGTAA 1980

1981 CCATTTTGATAATGCAACAATAAAGCATCTTCAGC 2015

00010927-091541

FIGURE 4
Homology of a Second IL-17 Human Receptor Like Polypeptide
Amino Acid Sequence (SEQ ID No: 5) and KNOWN Human IL 17
Receptor Family Mamber (SEQ ID NO: 3)

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1 MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLPDGLRDLRV 50
1 .....MGAARS 6
51 EPVTTTSVATGDYSILMNVSQVLR.ADASIRLL.KATKICVTGKSNFQSYS 98
|..|:|.|||:|:|:|
7 PP..SAVPGPLLGLLLLLLGVLPAGGASLRLLDHRALVCSQPGLNCTVKN 54
99 CVRLECSGAIMARCDLNLGSSDRSA.....SASRAAGTAGVGHQNWLI 142
|:|:|:|:|:|:|
55 STCLDDSW.IHPR...NLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTL 100
143 ....FVVFEVGGFTVLLVLNSSAQAICL..PRLPKVL..GLQWTFYSYIGF 184
:..|:|:|:|:|:|
101 QTDASILYLEGAELSVLQNTN.ERLCVRFEFLSKLRHHHRRWRFTFSHF 149
185 PVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCGLDHIMKYKKKCVKA 234
|:|. |:|:|. |:|:|:|:|:|
150 VVDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSS 199
235 GSLWDPNITACKKNEETVEVNFTTTPLGNRYMALI.....QHSTIIGF 277
|||||:|:|:|:|:|
200 GSLWDPNITVETLEAHQLRVSFTLWNETHYQILLTSFPHMENHSCFEHM 249
278 SQVFEPHQKQTRASVVIPVTGDSEGA...TVQLTPYFPTCGSDCIRHKG 324
:|..|:|:|:|:|:|:|
250 HHIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFSSCLNDCLRHS 299
325 TVVLCPO.TGVPFPLDNNKSKPGGWLPLLLLSLLVATWVLVAGIYLMWRH 373
|:|:|:|:|:|:|:|:|
300 T.VSCPEMPDTPEPIPDYMWVWF.ITGISILLVGSVILLIVCMTWRL 347
374 ERIKTSFSTTT.....LLP....PIKVLVVYPSE.ICFHHTICY 408
:|:|:|:|:|:|:|
348 AGPGSEKYSDDTKYTDGLPAADLIPPLKPRKVWIIYSADHPLYVDVVLK 397
409 FTEFLQNHCRSEVILEKWQKKKIAEMGPVQWLATQK...KAADKVVFL 454
|:|:|:|:|:|:|:|:|
398 FAQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIIVLC 447
455 SNDVNSVCDGTCGKSEGSP.....SENSQDLFPLAFNLFCSDLRSQIH 497
|:|:|:|:|:|:|:|
448 SRGTRAKWQALLGR..GAPVRLRCDHGKPVGDLFTAAMNMILPDFKRPAC 495
498 LHKYVVVYFREIDTKDDY.NALSVCPKYHLMK..DATAFCAELLHVKKQV 544
|||:|:|:|:|:|:|
496 FGTYVVCYFSEVSCDGDVDFLFGAAPRYPLMDRFEEVYFRIQDLEMFQPG 545
545 SAGKRSQACHDGCCSL*..... 561
:|:|
546 RMHRVGELSGDNYLRSPGGRQLRAALDRFRDWQVRCPDWFECENLYSADD 595

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T0920-2607860

[illegible]

1 ATAAAAGCGCAGCGTGC GGGTGGCCTGGATCCCGCGCAGTGGCCCCGGCGATGTCTCGCTCGT 60
61 GCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCCGACCGTTCAATG 120
121 TGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCGGGAGA 180
181 CTTGAGGGACCTCCGAGTAGAACCTGTTACAACACTAGTGTTGCAACAGGGGACTATTCAAT 240
241 TTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGTGGACATTTTCTTACATCGGCTTCC 300
M W T F S Y I G F P -
301 CTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCCCATAATATTCCTAATGCAAATATGA 360
V E L N T V Y F I G A H N I P N A N M N -
361 ATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATAA 420
E D G P S M S V N F T S P G C L D H I M -
421 TGAAATATAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTT 480
K Y K K K C V K A G S L W D P N I T A C -
481 GTAAGAAGAATGAGGAGACAGTAGAAGTGAACCTCACAACCACTCCCTGGGAAACAGAT 540
K K N E E T V E V N F T T T P L G N R Y -
541 ACATGGCTCTTATCCAACACAGCACTATCATCGGGTTTTTCTCAGGTGTTTGAGCCACACC 600
M A L I Q H S T I I G F S Q V F E P H Q -
601 AGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTA 660
K K Q T R A S V V I P V T G D S E G A T -
661 CGGTGCAGCTGACTCCATATTTTCTACTTGTGGCAGCGACTGCATCCGACATAAAGGAA 720
V Q L T P Y F P T C G S D C I R H K G T -
721 CAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAAAAGCAAGC 780
V V L C P Q T G V P F P L D N N K S K P -
781 CGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGTGG 840
G G W L P L L L L S L L V A T W V L V A -
841 CAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCA 900
G I Y L M W R H E R I K K T S F S T T T -
901 CACTACTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCATCACA 960
L L P P I K V L V V Y P S E I C F H H T -
961 CAATTTGTTACTTCACTGAATTTCTTCAAACCATTGCAGAAGTGAGGTCATCCTCGAAA 1020
I C Y F T E F L Q N H C R S E V I L E K -
1021 AGTGGCAGAAAAAGAAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAGA 1080
W Q K K K I A E M G P V Q W L A T Q K K -
1081 AGGCAGCAGACAAAGTCGTCTTCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGGTA 1140
A A D K V V F L L S N D V N S V C D G T -
1141 CCTGTGGCAAGAGCGAGGGCAGTCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCTT 1200
C G K S E G S P S E N S Q D L F P L A F -
1201 TTAACCTTTTCTGCACTGATCTAAGAAGCCAGATTTCATCTGCACAAATACGTGGTGGTCT 1260
N L F C S D L R S Q I H L H K Y V V V Y -
1261 ACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACC 1320
F R E I D T K D D Y N A L S V C P K Y H -

1MWTFSYIGFP	10
101	QTDASILYLEGAELSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFV	150
11	VELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYKKKCKVKAG	60
151	VDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSSG	200
61	SLWDPNITACKKNEETVEVNFTTTPLGNRYMALI.....QHSTIIGFS	103
201	SLWDPNITVETLEAHQLRVSFLLWNETHYQILLTSFPHMENHSCFEHMH	250
104	QVFEPHQKKQTRASVVIPVTGDSEGA...TVQLTPYFPTCGSDCIRHKGT	150
251	HIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFSSCLNDCLRHSAT	300
151	VVLC PQ.TGVPFPLDNNSKPGGWLPLLLLLSLLVATWVLVAGIYLMWRHE	199
301	.VSCPEMPDTPEPIPDYMLVWYWF.ITGISILLVGSVILLIVCMTWRLA	348
200	RIKKTSTSTTT.....LLP...PIKVLVVPYSE.ICFHHTICYF	234
349	GPGSEKYSDDTKYTDGLPAADLIPPLKPRKVWIIYSADHPLYVDVVLKF	398
235	TEFLQNHCRSEVILEKWQKKKIAEMGPVQWLATQK...KAADKVVFLLS	280
399	AQFLLTACGTEVALDLLLEEQAISEAGVMTWVGROKQEMVESNSKIIVLCS	448
281	NDVNSVCDGTCGKSEGSP.....SENSQDLFPLAFNLFCSDLRSQIHL	323
449	RGTRAKWQALLGR..GAPVRLRCDHGKPVGDLFTAAMNMILPDFKRPACF	496
324	HKYVVVYFREIDTKDDY.NALSVCPKYHLMK..DATAFCAELLHVKKQVS	370
497	GTYVVCYFSEVSCDGDVPLDFGAAPRYPLMDRFEEVYFRIQDLEMFQPGR	546
371	AGKRSQACHDGCCSL*.....	386
547	MHRVGELSGDNYLRSPPGGRQLRAALDRFRDWQVRCPDWFECENLYSADDQ	596

FIGURE 7
Overlap of Amino Acid Sequences of the First (SEQ ID NO: 2),
Second (SEQ ID NO: 5), and Third (SEQ ID NO: 7) Human IL-17
Receptor Like Polypeptides

1	MSLVLLSLAA	LCRS	AVPREP	TVQCGSETGP	SPEWMLQHDL	IPGDLRDLRV
1	MSLVLLSLAA	LCRS	AVPREP	TVQCGSETGP	SPEWMLQHDL	IPGDLRDLRV
51	EPVTTSVATG	DYSILMNVS	W	VLRADASIRL	LKATKICVTG	KSNFQSYSCV
51	EPVTTSVATG	DYSILMNVS	W	VLRADASIRL	LKATKICVTG	KSNFQSYSCV
101	RCNYTEAFQT	QTRPSGGK--	-----	-----	-----	-----
101	RLECSGAIMA	RCDLNLGSS	DRSASASRAA	GTAGVGHQNW	LIFVVVFVEGG	
119	-----	-----	-----WTFS	YIGFPVELNT	VYFIGAHNIP	
151	FTVLLVLNSS	AQAICLPRLP	KVLGLQWTF	YIGFPVELNT	VYFIGAHNIP	
1			MWTF	YIGFPVELNT	VYFIGAHNIP	
143	NANMNEDGPS	MSVNFTSPGC	LDHIMKYKKK	CVKAGSLWDP	NITACKKNEE	
201	NANMNEDGPS	MSVNFTSPGC	LDHIMKYKKK	CVKAGSLWDP	NITACKKNEE	
26	NANMNEDGPS	MSVNFTSPGC	LDHIMKYKKK	CVKAGSLWDP	NITACKKNEE	
193	TVEVNFTTTP	LGNRYMALIQ	HSTIIGFSQV	FEPHQKKQTR	ASVVIPVTGD	
251	TVEVNFTTTP	LGNRYMALIQ	HSTIIGFSQV	FEPHQKKQTR	ASVVIPVTGD	
76	TVEVNFTTTP	LGNRYMALIQ	HSTIIGFSQV	FEPHQKKQTR	ASVVIPVTGD	
243	SEGATVQLTP	YFPTCGSDCI	RHKGTTVLCP	QTGVPPFLDN	NKSKPGGWLP	
301	SEGATVQLTP	YFPTCGSDCI	RHKGTTVLCP	QTGVPPFLDN	NKSKPGGWLP	
126	SEGATVQLTP	YFPTCGSDCI	RHKGTTVLCP	QTGVPPFLDN	NKSKPGGWLP	
293	<u>LLLLSLLVAT</u>	<u>WVLVAGIYLM</u>	<u>WRHERIKKTS</u>	<u>FSTTTLLPPI</u>	<u>KVLVVYPSEI</u>	
351	<u>LLLLSLLVAT</u>	<u>WVLVAGIYLM</u>	<u>WRHERIKKTS</u>	<u>FSTTTLLPPI</u>	<u>KVLVVYPSEI</u>	
176	<u>LLLLSLLVAT</u>	<u>WVLVAGIYLM</u>	<u>WRHERIKKTS</u>	<u>FSTTTLLPPI</u>	<u>KVLVVYPSEI</u>	
343	CFHHTICYFT	EFLQNHCRSE	VILEKWQKKK	IAEMGPVQWL	ATQKKAADKV	
401	CFHHTICYFT	EFLQNHCRSE	VILEKWQKKK	IAEMGPVQWL	ATQKKAADKV	
226	CFHHTICYFT	EFLQNHCRSE	VILEKWQKKK	IAEMGPVQWL	ATQKKAADKV	
393	VFLLSNDVNS	VCDGTCGKSE	GSPSENSQDL	FPLAFNLFCS	DLRSQIHLHK	
451	VFLLSNDVNS	VCDGTCGKSE	GSPSENSQDL	FPLAFNLFCS	DLRSQIHLHK	
276	VFLLSNDVNS	VCDGTCGKSE	GSPSENSQDL	FPLAFNLFCS	DLRSQIHLHK	
443	YVVVYFREID	TKDDYNALSV	CPKYHLMKDA	TAFCAELLHV	KQQVSAGKRS	
501	YVVVYFREID	TKDDYNALSV	CPKYHLMKDA	TAFCAELLHV	KQQVSAGKRS	
326	YVVVYFREID	TKDDYNALSV	CPKYHLMKDA	TAFCAELLHV	KQQVSAGKRS	
493	QACHDGCCSL	*				
551	QACHDGCCSL	*				
376	QACHDGCCSL	*				

Figure 8

Northern Blot Expression Analysis of TH00-018
Necropsied Transgenic Founders

0.54 kb →

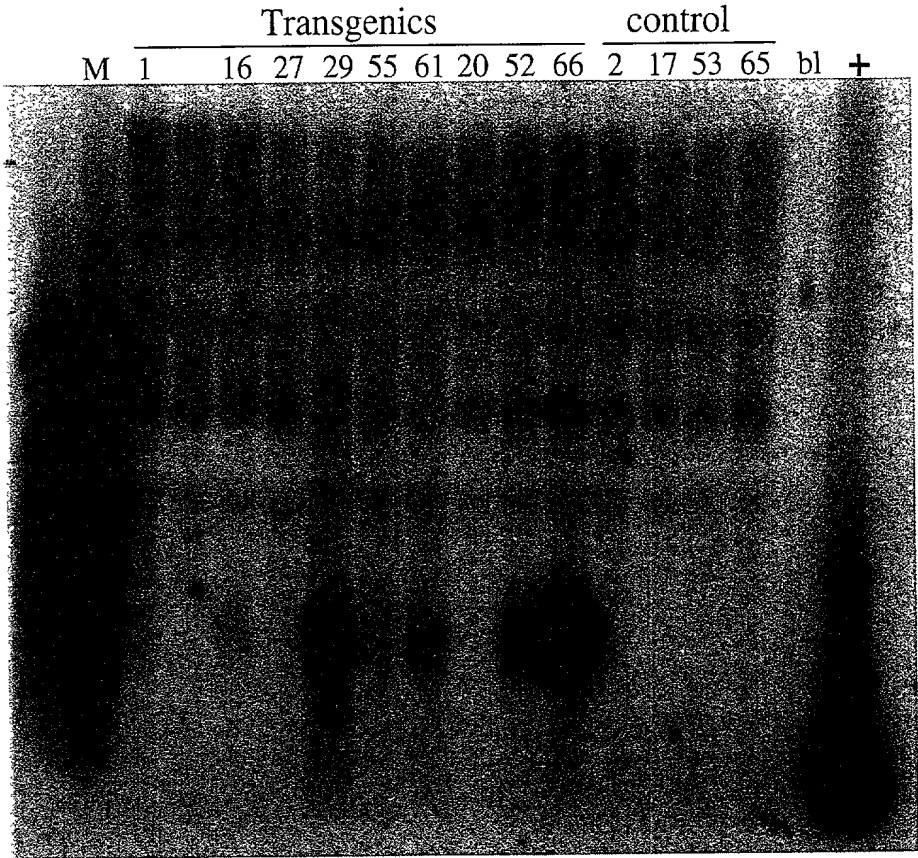


Figure 9

Northern Blot Expression Analysis of TH00-018
Necropsied Transgenic Founders

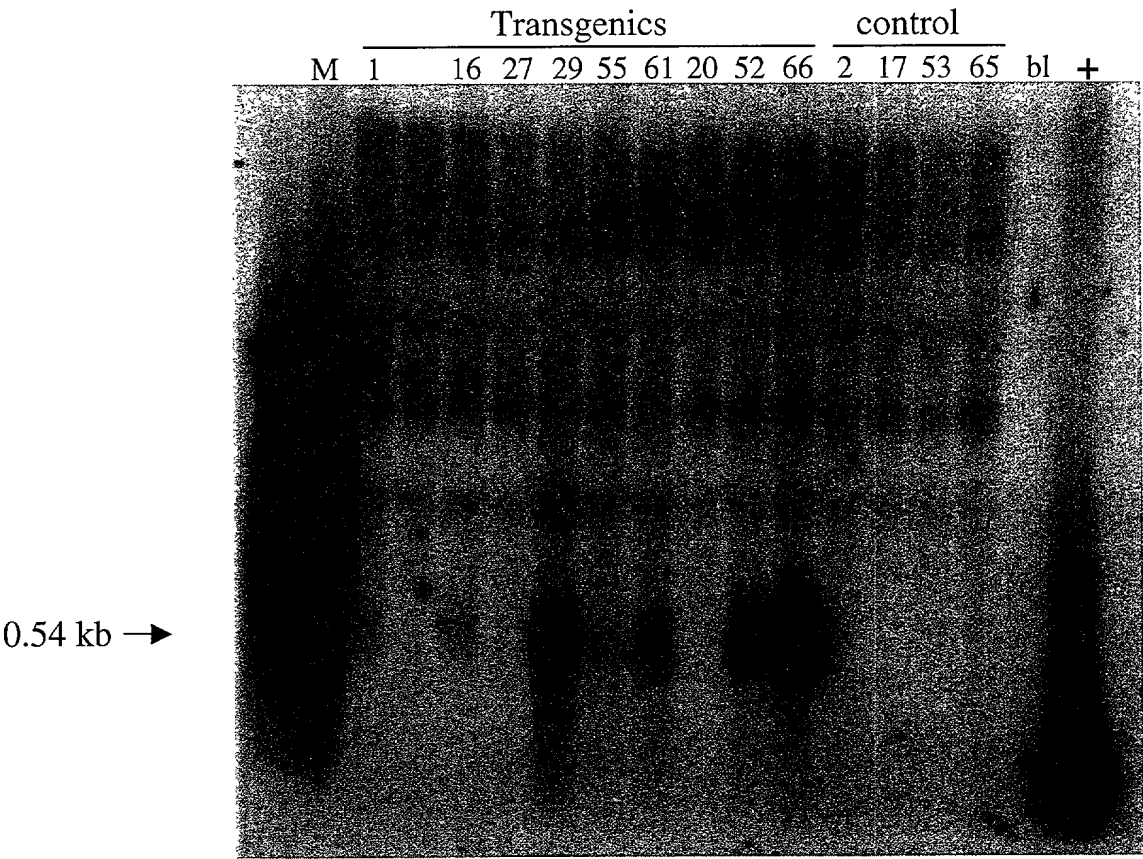


Figure 10

Non-Transgenics

IL-17E Transgenics

A



B



Lymph Node H&E 2x

C



D

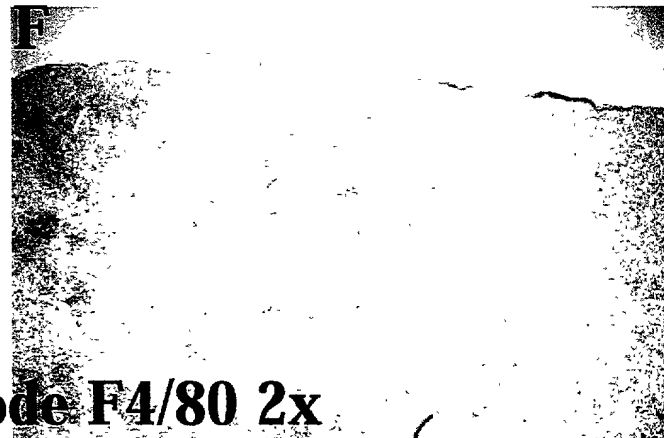


Lymph Node B220 2x

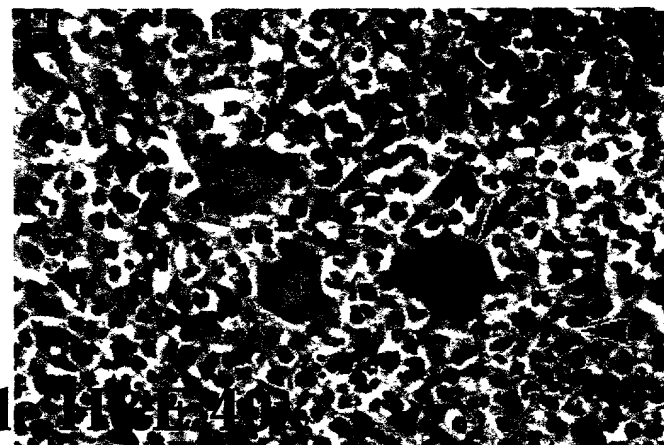
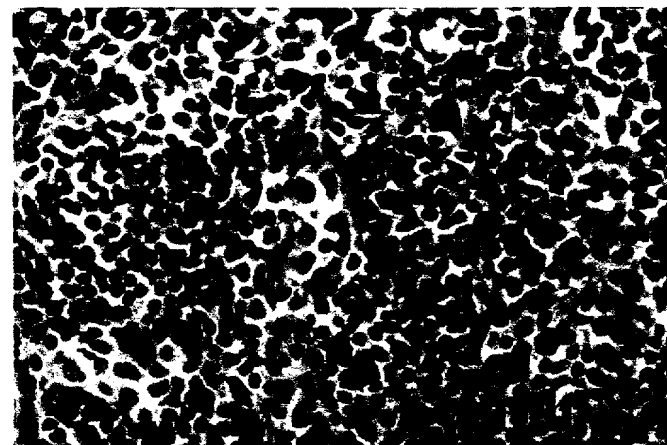
E



F



Lymph Node F4/80 2x



Lymph Node H&E 40x

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Figure 11

Non-Transgenics

IL-17E Transgenics

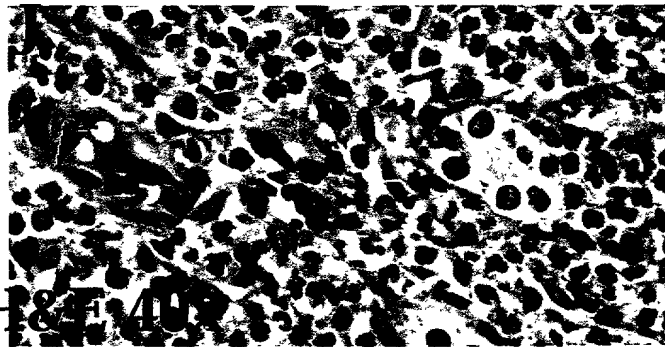
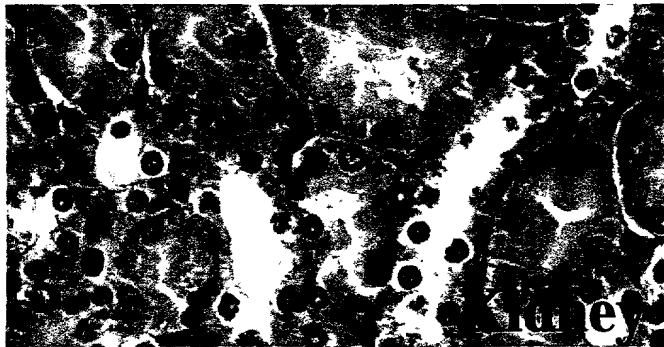
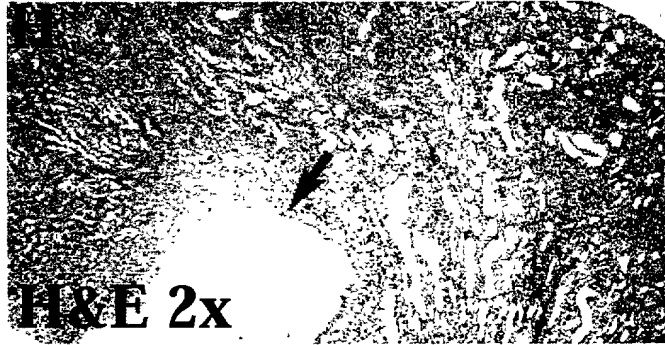
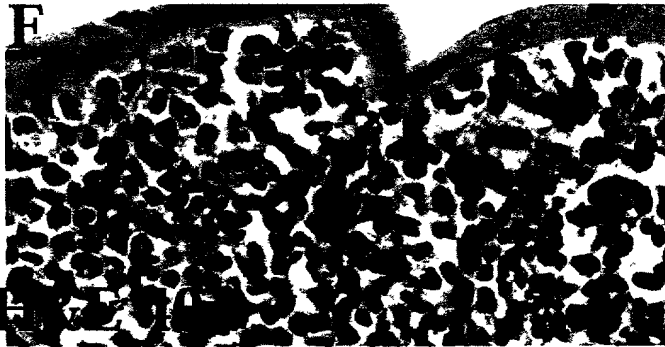
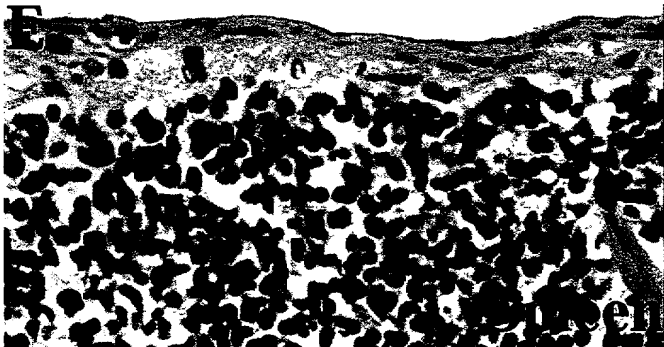
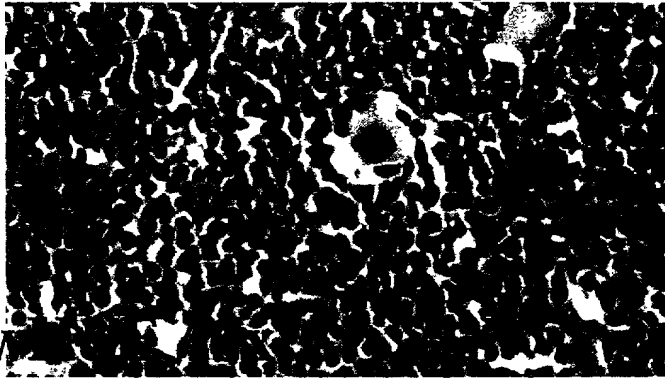
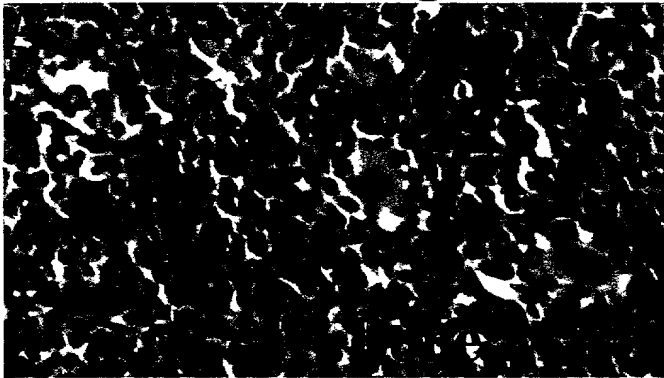


FIGURE 11

Figure 12

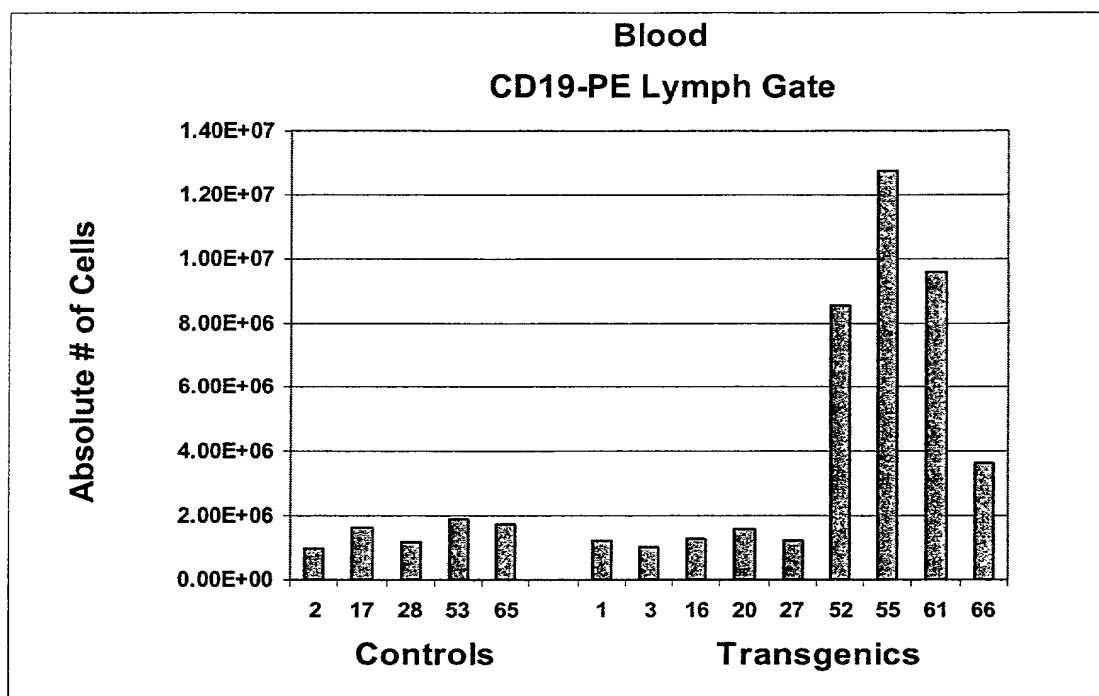


Figure 13

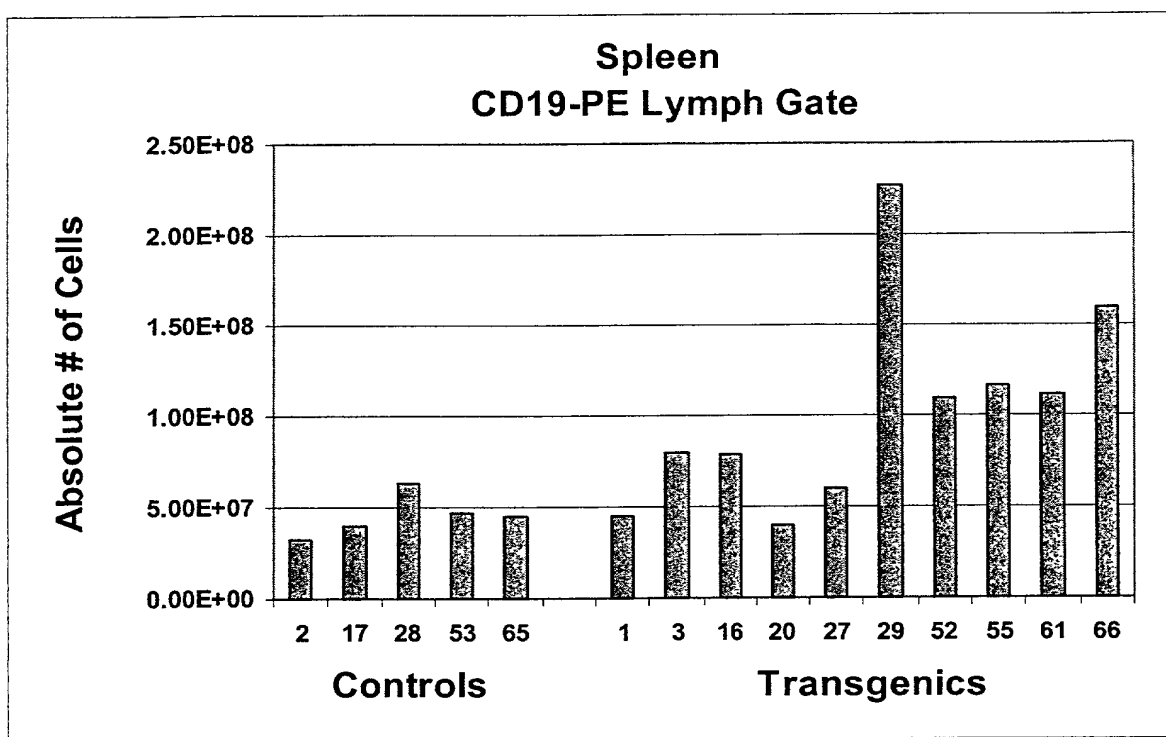


Figure 14

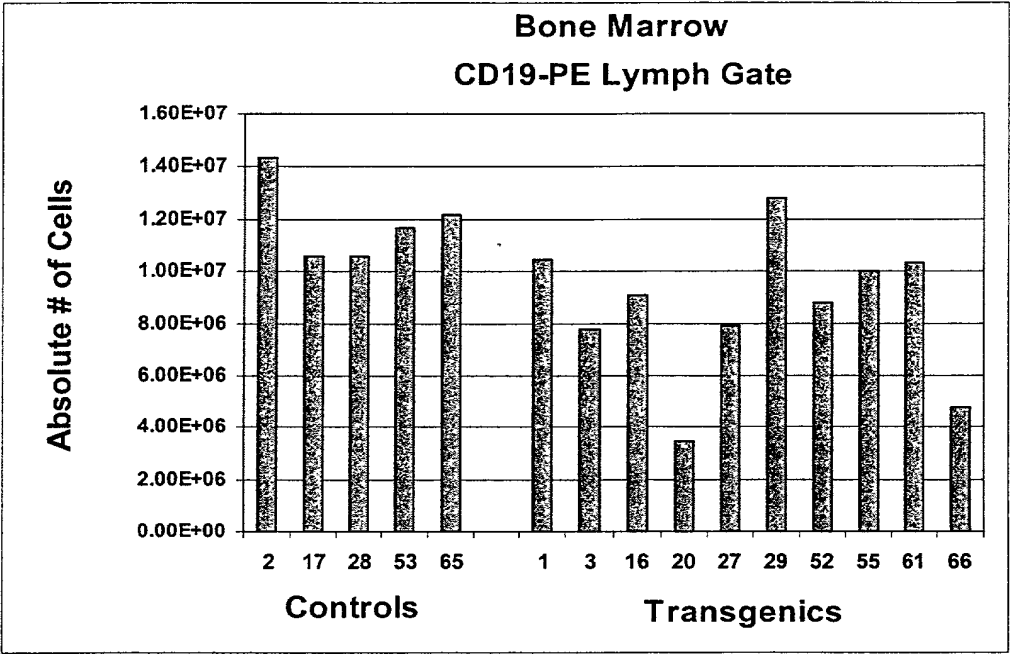


Figure 15

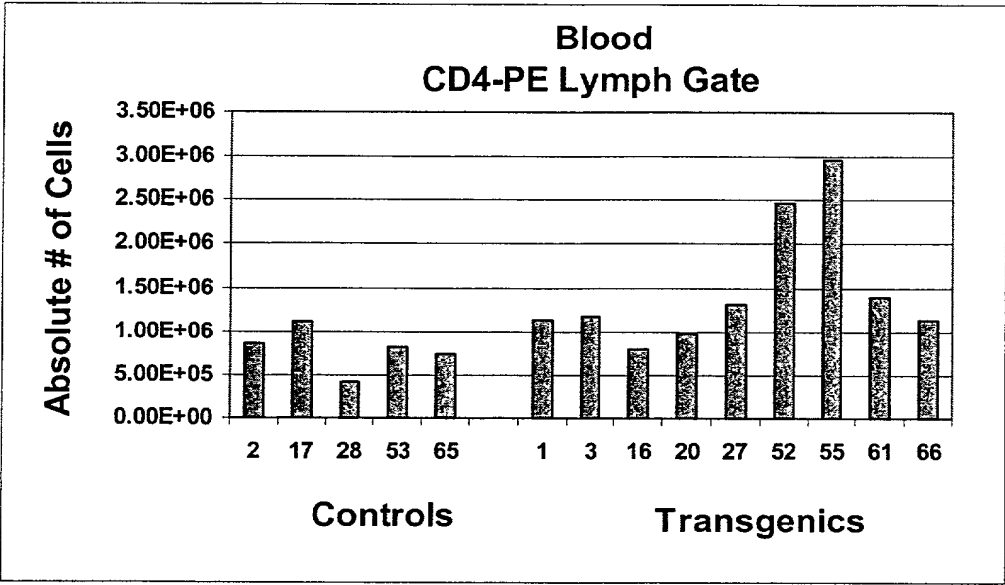


Figure 16

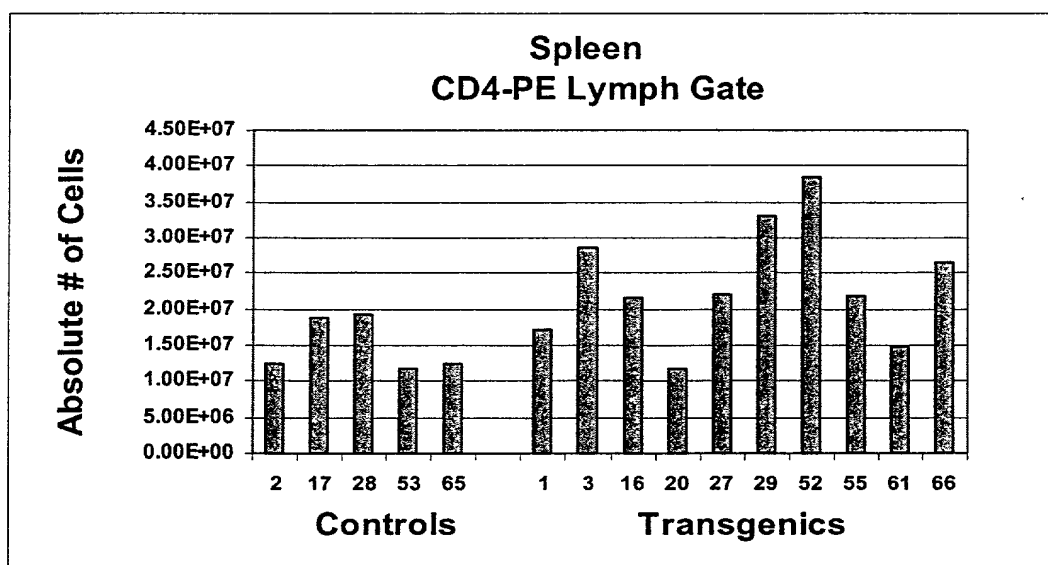


Figure 17

CD45R+ CELLS EXPRESSING IL17Br IN TRANSGENIC BONE MARROW

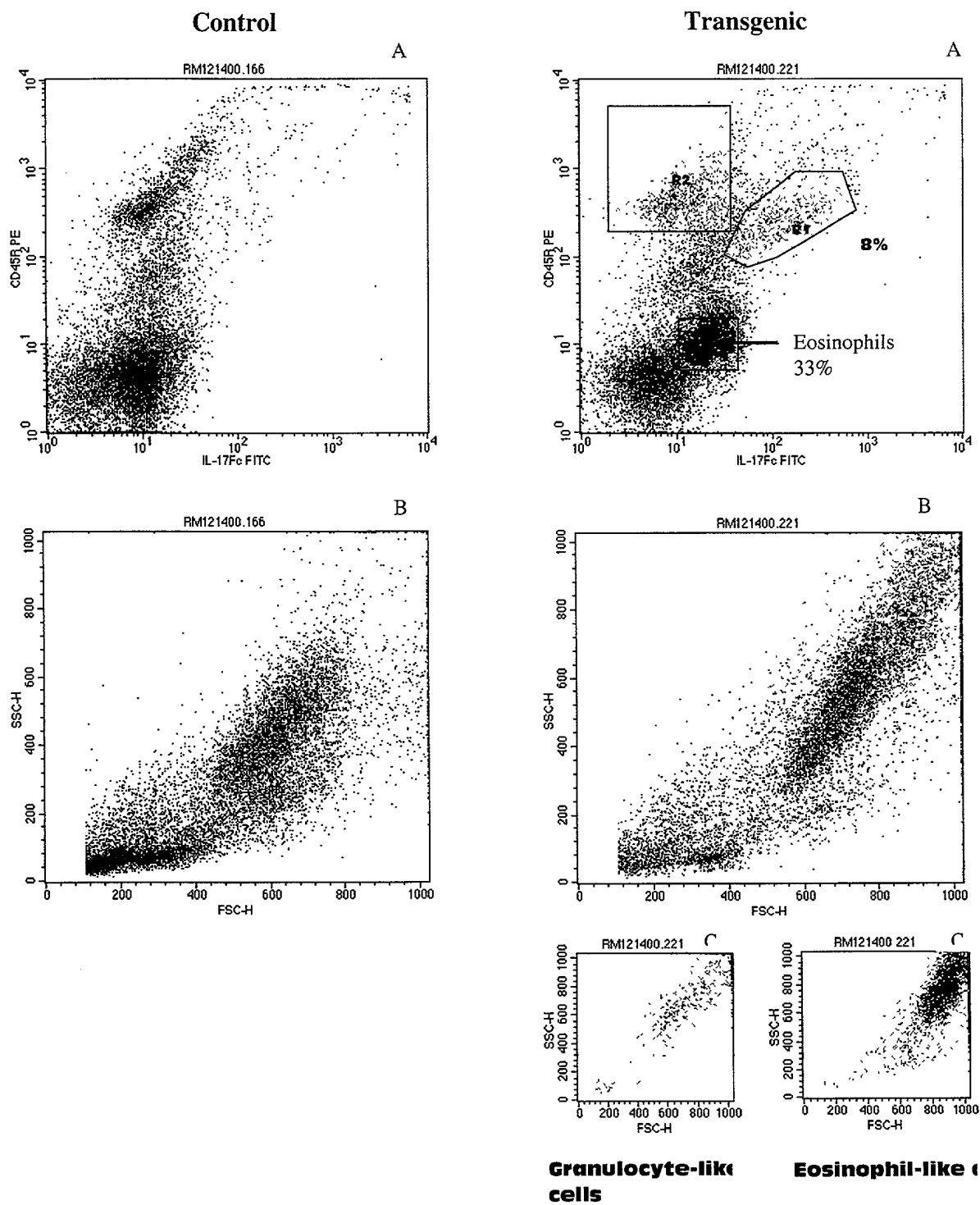
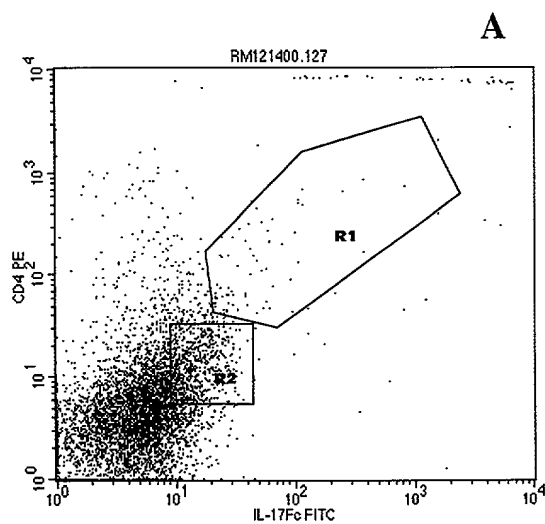
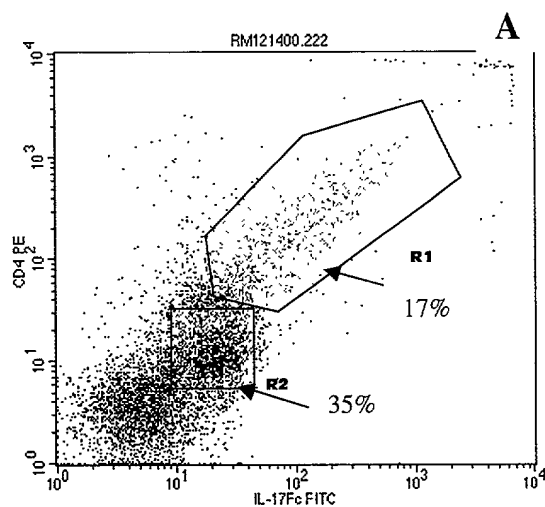


Figure 18

CD4+ CELLS EXPRESSING IL17Br IN TRANSGENIC BONE MARROW



CONTROL



TRANSGENI

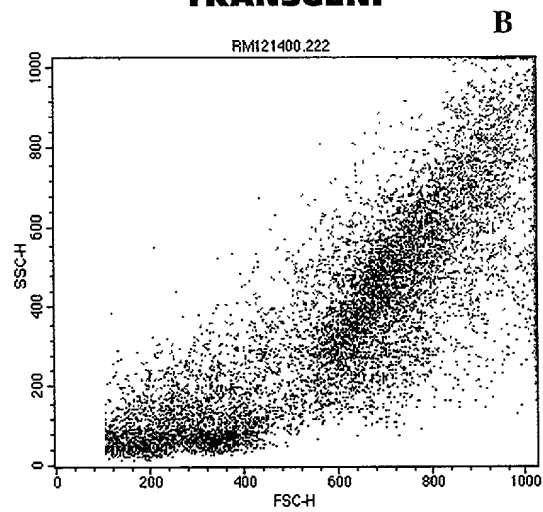
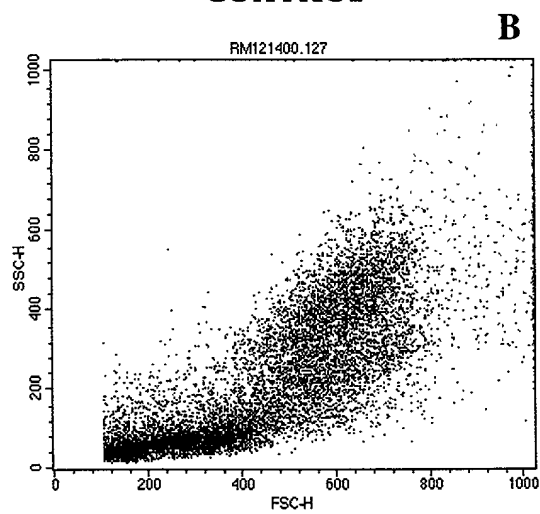


Figure 19

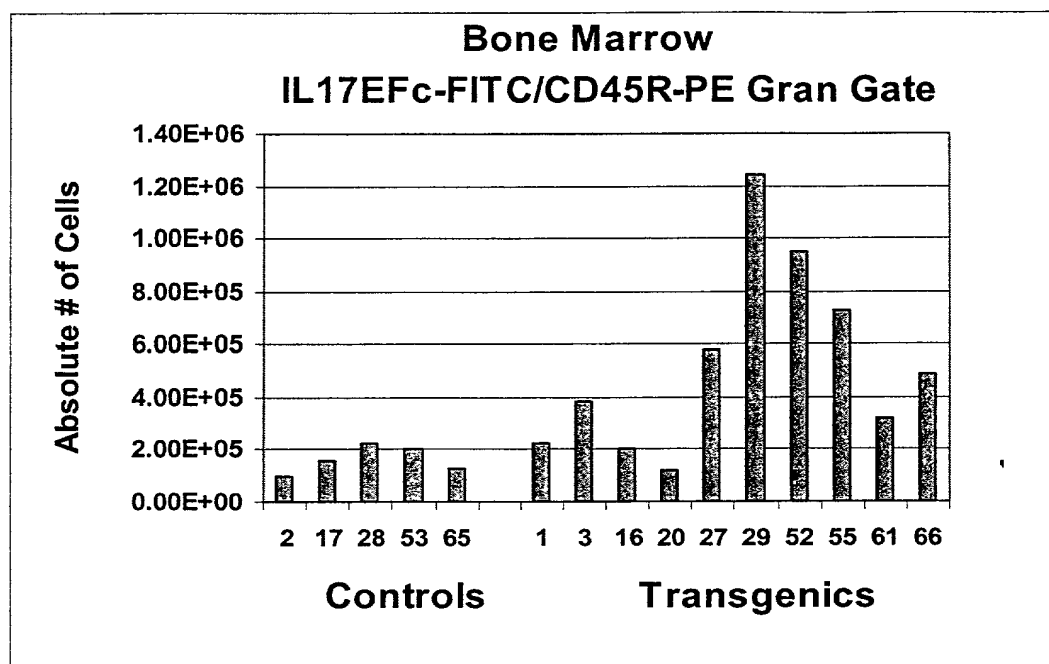


Figure 20

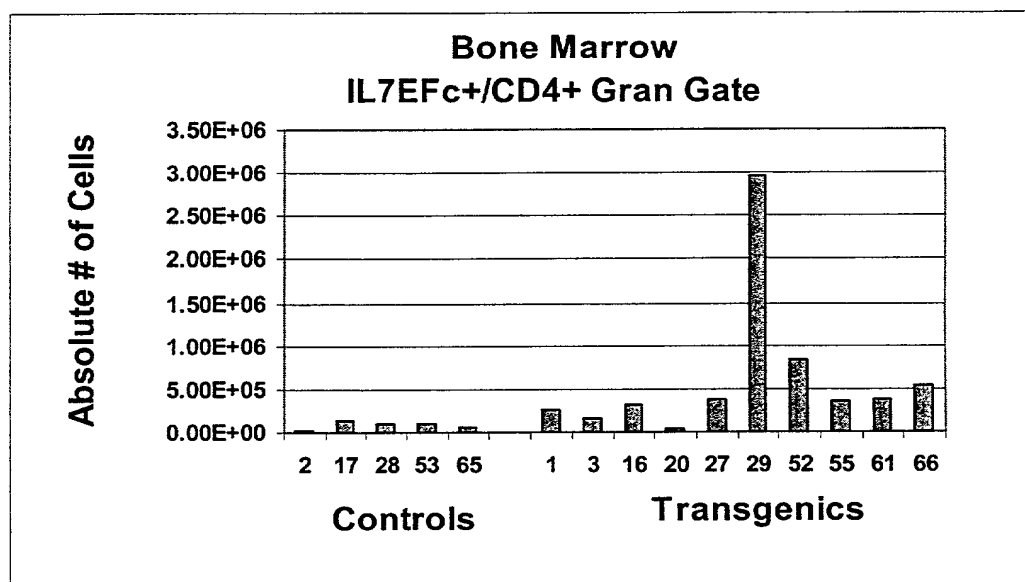


Figure 21

Example of a typical eosinophil Forward vs. Side scatter plot (size vs. granularity). Cells in the gate can be sorted to give a purified population.

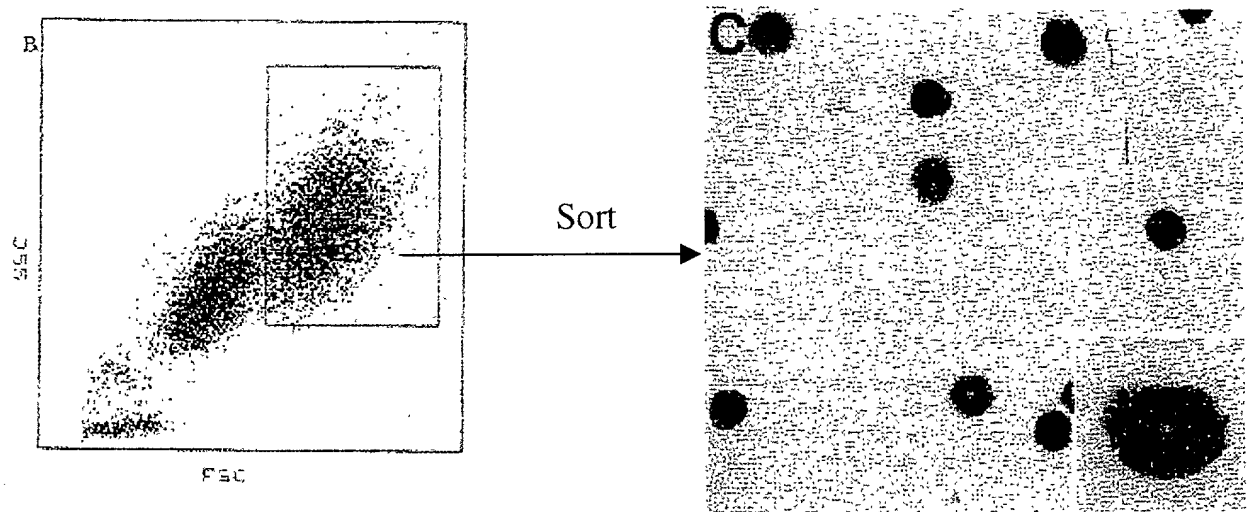


Figure 22

IL-17RB-2 Fusion Protein (SEQ ID NO: 24)

```
1      MSLVLLSLAA LCRSAVPREP TVQCGSETGP SPEWMLQHDL IPGDLRDLRV
51     EPVTTTSVATG DYSILMNVSF VLRADASIRL LKATKICVTG KSNFQSYSCV
101    RCNYTEAFQT  QTRPSGGKWT FSYIGFPVEL NTVYFIGAHN IPNANMNEDG
151    PSMSVNFTSP  GCLDHIMKYK KKCCKAGSLW DPNITACKKN EETVEVNFTT
201    TPLGNRYMAL IQHSTIIGFS QVFEPHQKKQ TRASVVIPVT GDSEGATVQL
251    TPYFPTCGSD CIRHKGTVVL CPQTGVFPPL DNNKSKPGGW LPAAAEPKSC
301    DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED
351    PEVKFNWYVD GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK
401    CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK NQVSLTCLVK
451    GFYPSDIAVE WESNGQPENN YKTTTPVLDS DGSFFLYSKL TVDKSRWQQG
501    NVFSCSVMHE ALHNHYTQKS LSLSPGK*
```

Figure 22

Figure 23

Fusion Protein for IL-17RB-3 (SEQ ID NO: 25)

1 **MSLVLLSLAA** **LCRS**AVPREP TVQCGSETGP SPEWMLQHDL IPGDLRLDRV
51 EPVTTSVATG DYSILMNVSF VLRADASIRL LKATKICVTG KSNFQSYSCV
101 RLECSGAIMA RCDLNLLGSS DRSASASRAA GTAGVGHQTW LIFVVFVEGG
151 FTVLLVLNSS AQAICLPRLP KVLGLQWTFS YIGFPVELNT VYFIGAHNIP
201 NANMNEDGPS MSVNFTSPGC LDHIMKYKKK CVKAGSLWDP NITACKKNEE
251 TVEVNFTTTP LGNRYMALIQ HSTIIGFSQV FEPHQKKQTR ASVVIPVTGD
301 SEGATVQLTP YFPTCGSDCI RHKGTVVLCP QTGVPPFLDN NKS~~K~~PGGWLP
351 AAAEPKSCDK THTCPPCPAP ELLGGPSVFL FPPKPKDTLM ISRTPEVTCV
401 VVDVSHEDPE VKFNWYVDGV EVHNAKTKPR EEQYNSTYRV VSVLTVLHQD
451 WLNGKEYKCK VSNKALPAPI EKTISKAKGQ PREPQVYTLPSRDELTKNQ
501 VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG SFFLYSKLTV
551 DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS LSPGK*

004097 2207860